

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 4)
Subject: gi|4557225 ref|NP_000005.1| alpha-2-macroglobulin precursor sp|P01023|A2MG_HUMAN ALPHA-2-MACROGLOBULIN
PRECURSOR (ALPHA-2-M) pir||MAHU alpha-2-macroglobulin precursor - human >gb|AAA51551.1| (M11313) alpha-2-macroglobulin
precursor [Homo sapiens] (SEQ ID NO: 23)
Length = 1474

Score = 2714 (960.4 bits), Expect = 1.7e-281, P = 1.7e-281
Identities = 596/1494 (39%), Positives = 874/1494 (58%)

Query: 13 LLLGMLALSPAIAEELPNVLTLPARLNPFSVQKVCLDLSPGYSDVKFTVTLETCKDTQK 192
 LLL +L +++ + P Y+V +P+ L+ + +K C+ LS V + +LE+ +
Sbjct: 14 LLLVLLPTDASVSGK-PQYMLVLPSSLHTTETTEKGCVLLSYLNETVTVSASLESVRGNRS 72

Query: 193 LLEYSGLKKRHLHCISFLVPPAGTGEVATIRVSGVGNNISFEEKKKVLIQRQNGTFV 372
 L + LHC++F VP + EEV + V G F+++ V+++ + + FV
Sbjct: 73 LFTDLEAENDVLHCVAFAPK-SSSNEEVNFLTQVQKGPTQEFKKRTTVMVKNEDSLFPV 131

Query: 373 QTDKPLYTPGQQVYFRIVTMDSNFVNDKYSMVLELQDPNSNRIQAQWLEVVPEQGIVDLS 552
 QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIQOW E G+ S
Sbjct: 132 QTDKSIYKPGQTVKFRVVSMDENFHLNELPLVYIQDPKGNRIQAQWQSFLEGGKQFS 191

Query: 553 FQLAPEAMLGTYTVAE---GKTFGTFSEHYVLPKFKVEVVEPKELSTVQESFLVKIC 723
 F L+ E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ ++E V +C
Sbjct: 192 FPLSSEPFQGSYKVVVQKKSGGRTEHPFTVEEFVLPKFEVQTVPKIITILEEMNVSV 251

Query: 724 CRYTYGKPMGLGAVQSVQCQKANTYVREVEREQLPDKCRNLSGQTDKTCGCFAPVDMATF 903
 YTYGKP+ G V VS+C+K + + E C SGQ + GCF V F
Sbjct: 252 GLTYGKPVPGHVTVSICRKYSDA--SDCHGEDSQAFCEKFSGQLNSHGCFYQQVKTVF 309

Query: 904 DLIGYAYSHQINIVATVVEEGTGVANATQNIYISPMGSMTFEDTSNFYHFNFPFSGKI 1083
 L Y +++ A + EGT VE Q+ I+ + ++F + + PF G++
Sbjct: 310 QLRKKEYEMKLHTEAQIQEETVVVELTGRQSSSEITRTITKLSFVKVDSHFRQGIPIFFGQV 369

Query: 1084 RVRGHDDSFLLKNHLVFLVIYGTNGTFNQTLVTDNNGIAPFTLETSGWNGTDVSLGKFQM 1263
 R+ + N ++F I G + TD +GL F++ T+ GT +++ ++
Sbjct: 370 RLVDGKGVPIPNKVIF--IRGNEANYYSNATTDHGLVQFSINTTNVMGTSLTVRVNYKD 427

Query: 1264 EDLVNPEQVPRYQNAYLHLRPFYSTRTSFLGTHRLNGPLKCGQPQEVLDVYIDPADA 1443
 Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++
Sbjct: 428 RSPCYGYQWVSEEEHAHTAYLVFSPSKSFVHLEPMSHELPCGHTQTVQAHYILNGGTL 487

Fig 1A

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23

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Query: 1444 SPDQEIFSYLIGKGLVMEQKHLNKKKGLKASFSLSLTFTSRLAPDPSLVIYAIFF 1623
      +++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P
Sbjct: 488 LGLKKLSFYLLIMAKGGIVRTGTHLLVKQEDMKGHFSISIPVKS DIAAPVARLLIYAVLP 547

Query: 1624 SGGVVADKIQFSVGMCFDQVSLGFSFSPSQLPAGAEVELQLQAAPGSLCALRAVDSESVLLL 1803
      +G V+ D ++ V C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1804 RPDRELSNRSVYGMFPFWYGHYPYQYAEVQCPVSGPWFDPQLIDPMPQGHSSQRSIIW 1983
      +PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KPDAELSASSVYNLLP-----EKDLTGFPGPLN-DQDDEDCINRHNVIYINGITY 655

Query: 1984 RP-SFSEGTDLFSFFRDVGLKILSNAKIKKVPDCSH-----RSPE-----YSTAMGGG 2124
      P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSSSTNEKDMYSFLEDMLKAPTNSKIRKPKMCPQLQYEMHGPEGLRVGFYESDVNGR 715

Query: 2125 GHPEAFESSTPLHQAEDSQVROYFPETWLWDLFPIGNSGKEAVHVTVPDAITEMKAMSF 2304
      GH P H VR+YFPETW+WDL + ++G V VTVPD ITEMKA +FC
Sbjct: 716 GHARLVHVEEP-HT---ETVRKYFPETWIWDLVVVNSAGVAVGVTPDITTEMKAGAF 771

Query: 2305 TSQSRGFLSPTVGLTAFKPPFFVDLTLPSVVRGESFRLTATIFNYLKDCIRVQTDLAKS 2484
      S+ G G+S T L AF+PFFV+LT+PYSV+RGE+F L AT+ NYL CIRV L S
Sbjct: 772 LSEDAGLGISSTASLRAFQPPFFVELTMPYSVIRGEAFTLKATVNLNYLPKCIRVSVQLEAS 831

Query: 2485 HEYQLESWADSQTSCLCADDKTHHWNITAVKLGHINFITSTKILDSNEPCGQKGFVP 2664
      + Q C+CA+ +T W +T LG++NFT+S + L+S E CG + VP
Sbjct: 832 PAFLAVPVEKEQAPHCICANGRQTVSWAVTPKSLGNVNFVTSABALESQELCGTEVPSPV 891

Query: 2665 QKGRSDTLIKPVLVKEGVLVVEKTHSSLLCPKGVASESVSLELPVDIVPDSTKAYVTVL 2844
      + GR DT+IKP+LV+PEG+ E T +SLTCP G SE +SL+LP ++V +S +A V+VL
Sbjct: 892 EHGRKDTVIKPLLVPEPEGLEKETTFNSLLCPSGGSEVSEELSLKLPNPNVVEESARASVSVL 951

Query: 2845 GKQLEILDSEKRRMEAAKVWRDINGTALQNLQVMPSGCGEQNMVLFAPLIYVLQYL 3024
      G DI+G+A+QN L+QMP GCGEQNMVLFAP IYVL YL
Sbjct: 952 G-----DILGSAMQNTQNLQMPYCGCGEQNMVLFAPNIYVLQYL 990

Query: 3025 EKAGLTTEEIRSAVGFLFEGYQKELMKHNSYSYAFGERDGN--GNTWLTAFVTKCFG 3198
      + LT E++S+A+G+L GYQ++L YKH +GSYS FGER G GNTWLTAFV K F
Sbjct: 991 NETQQLTPEVKS KAIGYLN TGYQRLNKKHYDGSYSTFGERYGRNGNTWLTAFVTKTFA 1050

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Fig. 1B

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23**

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Query: 3199 QAQKFIFIDFNIDALWKMGAGNQLPSGCYANVGNLLHTAMKGGVDDVSLTAVVTAALL 3378
      QA+ +IFID +I AL W++ Q +GC+ + G+LL+ A+KGV+DEV+L+AY+T ALL
Sbjct: 1051 QARAYIFIDEAHITQALIWLSQRQKNGCFRSSGSLNNAIKGVEDEVTL SAYITIAL 1110

Query: 3379 EMGKDVEDPMVSGLRCLKNSATST-----TNLYTQALLAYIFSLAGEMDIRNILLKQ 3537
      E+ V P+V L CL+ SA T +++YT+ALLAY F+LAG D R +LK
Sbjct: 1111 EPLTVTHFVVRNALFCLE-SAMKTAQEGDHGSHVYTKALLAYAFALAGNQDKRKEVLKS 1169

Query: 3538 LDQQAIIISGESIYWSQKPTRSSNASPWSEPA--VDVELTAYALLAQLT-KPSLTQKEIA 3708
      L+++A+ S++W + P + + EP A +VE+T+Y LLA LT +P+ T +++
Sbjct: 1170 LNEEAVKKDNSVHWERPQKPKAPVGHFYEPOAPSAEVEMTSYVLLAYLTAQPAPTSEDLT 1229

Query: 3709 KATSIVAWLAKQHNAYGGFSSQTQDTWVALQALAKY-ATTAYMPSEEINLVVKSTENFQRT 3885
      AT+IV W+ KQ NA GGFSSQTQDTWVAL AL+KY A T + + ++S+ F
Sbjct: 1230 SATNIVKWIITKQNAQGGFSSQTQDTWVALHALSKYGAATFRTGKAAQVTIQSSGTFSSK 1289

Query: 3886 FNIQSVNRLVFOQDTLPNVPGMYTLEASGQGCYVYVQTVLRYNILPPTNMKTFSLSVEIGK 4065
      F + + NRL+ QQ +LP +PG Y+++ +G+GVY+QT L+YNILP F+L V+
Sbjct: 1290 FQVDNNRLLQQVSLPELPGEYSMKVTGEGCVLQTSLYKNILPEKEEFPFALGVQTL 1349

Query: 4066 ARCEQPTSPRSLTLTIHTSYVGSRSSNNMAIVEVKMLSGFSPMEGTNQLLQQPLVKVE 4245
      C++P + S +++ SY GSR+SNMAIV+VKM+SGF P++ T ++L + V + E
Sbjct: 1350 QTCDEPKAHTSFQISLSVSYTGSRASNNMAIVDKMVSGFIPKPTVKMLERSNHVSRTE 1409

Query: 4246 FGTDPLNIYLDLILKNTQTYTFTISQSVLVTNLKPAATIKVVDYVLPGSFKLSQY 4407
      ++ + IYLD++ T + FT+ Q V +LKPA +KVDYV F +++Y
Sbjct: 1410 VSSNHVLIYLDKVSQNTLSLFFTVLQDVPVRDLKPAIVKVVVDYETDEFAIAEY 1463

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FIG. 1C

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 4)
 Subject: sp|R11334|R11334 Recombinant human alpha-2 macroglobulin. (SEQ ID NO 24)
 Length = 1474

Score = 2699 (955.2 bits), Expect = 3.2e-280, P = 3.2e-280
 Identities = 596/1494 (39%), Positives = 870/1494 (58%)

Query:	13	LLGLMLALSPAIAELPNYLVTLPARLNFPSVQKCLDLSPGYSDVKFTVTLETCKDTQK	192
		LLL +L + A P Y+V +P+ L+ + +K C+ LS V + +LE+ +	
Sbjct:	13	LLLLVLPTDASVSGKPQYQYMLVPSLLHTETETKGCVLLSYLNETVTVSASLESVRGNS	72
Query:	193	LLSYGLKKRHLHCISFLVPPPPAGGTEEVATIRVSGVGNNISFEKKKVLIIQROGNGTFV	372
		L + LHC++F VP + EEV + V G F+++ V+++ + + FV	
Sbjct:	73	LFTDLAENDVLHCVAFAVPK-SSSNEEVMLFTVQVKGPTQEFKKRTTVMVKNEDSLVFV	131
Query:	373	QTDKPLYTPGQYVFRIVTMDSNFVPVNDKYSMVLELQDPNSNRIQAOWLEVPEQGIVDLS	552
		QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIAQW E G+ S	
Sbjct:	132	QTDKSIYKPGQTVKFRVSMDFNPHLPLVYIQDPKGNRIQAOWQSFQLEGGKQFS	191
Query:	553	FQLAPEAMLGTYTVAAE--GKTFGTFSVEEYVLPKFKVEVPEPKELSTVQESFLVKIC	723
		F L+ E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ ++E V +C	
Sbjct:	192	FPLSEPFQGSYKVVVQKSGGRTEHPFTVEEFVLPKFVQVTVPKIITILEEMNVSV	251
Query:	724	CRYTYGKPMGLGAVQSVQKANTYMYREVEREQLPDKCRNLSGQTDKTCFSAVDMATF	903
		YTYGKP+ G V VS+C+K + E C SGQ + GCF V F	
Sbjct:	252	GLTYGKPVPGHVTVSICRKYSDA--SDCHGEDSQAFCEKFSQNLNSHGCFYQQVKT	309
Query:	904	DLIGYAYSHQINIVATVVEEGTGVANATQNIYISPMGSMTFEDTSNFYHPNFPFSGKI	1083
		L Y +++ A + EGT VE Q+ I+ + ++F	
Sbjct:	310	QLKRKEYEMKLHTEAQIQEEGTVVVELTGRQSEITRTITKLSFVKVDSHFQGIPIFFGQV	369
Query:	1084	RVRGHDDSFLLKNHLVFLVIYGTNGTFNQTLVTDNNGLAPFTLFTSGWNGTVDVSLGKFQM	1263
		R+ + N ++F I G + TD +GL F++ T+ GT +++ ++	
Sbjct:	370	RLVDGKGVPIPNKVIF--IRGNEANYYSNATTDDEHGLVQFSINTNMVMTSLTVRVNYKD	427
Query:	1264	EDLVNPEQVPRYQYQAYLHLRPFYSTRTSFLGIHRLNGPLKCGQPQEVLDYVIDPAD	1443
		Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++	
Sbjct:	428	RSPCYGYQWVSEHEEAHTAYLVSPKSFVHLEPMSHELPGHTQTQVAHYLLNGGTL	487
Query:	1444	SPDQETSFYYLIGKGLVMQKHLNSKKGLKASFSLSTFTSRLAPDPSLVYIAIFP	1623
		+++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P	
Sbjct:	488	LGLKKLSFYLLIMAKGGIVRTGTGHLVQEDMKGHFISIPVKSADIAPVARLLIYAVLP	547

Fig. 2A

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24

Query:	1624	SGGWADKIQFSVGMCFDNOVSLGFSQQLPGAELVQLQAAPGSLCALRAVDSESVLLL	1803
Sbjct:		+G V+ D ++ V C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+	
	548	TGDIVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTAAAPQSVCALRAVDQSVLLM	607
Query:	1804	RPDRELSNRSVYGMFPFWYGHYPYQVAEYDQCPVSGPWFPPQPLIDPMPQGHSSQRSIIW	1983
Sbjct:		+PD ELS SVY + P E D GP + Q D + + + I +	
	608	KPDAELSSASSVYNLLP-----EKDLTGFPGLN-DQDDEDCINRHNVIINGITY	655
Query:	1984	RP-SFSEGTDLFSFFRDVGLKILSNAKIKKPVDCSH-----RSP-----YSTAMGGG	2124
Sbjct:		P S + D++SF D+GLK +N+KI+KP C PE Y + + G	
	656	TPVSSSTNEKDMYSFLEDMGLKAF+NSKIRKPKMCPQLQYEMHGPEGLRVGFYESDVMMGR	715
Query:	2125	GHPEAFESSTPLHQAEDSQVRQYFPETWLDLFPFGNSGKEAVHVTVPDAITEWKAMSF	2304
Sbjct:		GH P H VR+VF ETW+MDL + ++G V VTVPD ITEMKA +FC	
	716	CHARLVHVEEP-HT---ETVRKYFAETWLDLVVNSAGVAEVGVTVPTITTEWKAGATC	771
Query:	2305	TSQSRGFGLSPTVGLTAFKPFVVDLTLPYSVVRGESFRLTATFNLYLDCIRVQTDLAKS	2484
Sbjct:		S+ G G+S T L AF+PFFV+LT+PYSV+RGE+F L AT+ NYL CIRV L S	
	772	LSEDAGLIGISTASLRAFQPFVVELTMPYSVIRGEAFTLKATVLYLPCIRVSVQLEAS	831
Query:	2485	HEYQLESWADSQTSCLCADDKTHHWNITAVKLGHINFITITKILDSNEPCGGQKGFVP	2664
Sbjct:		+ Q C+CA+ +T W +T LG++NFT+S + L+S E CG + VP	
	832	PAFLAVPEKEQAPHCICANGRQTVSWAVTFKSLGNVNFVSAEALQSQELCGTEVPSVP	891
Query:	2665	QKGRSDTLIKPVLVKEGVLVEKTHSSLLCPKGVASESVSLELPVDIVPDSTKAYVTVL	2844
Sbjct:		+ GR DT+IKP+LV+PEG+ E T +SLLC P G SE +SL+LP ++V +S +A V+VL	
	892	EHGRKDTVIKPLLVPEGLEKETTFNSLLCPSGGEVSEELSLKLPNNVVEESARASVSL	951
Query:	2845	GKQLEILDSEKRRRMEAAKVWRDIMGTLQNLQVMPSGCGEQNMVLFAPIIYVLQYL	3024
Sbjct:		G DI+G+A+QN L+QMP GCGEQNMVLFAP IYVL YL	
	952	G-----DILGSAMQNTQNLQMPYCGCGEQNMVLFAPNIYVLQYL	990
Query:	3025	EKAGLLTEEIRSAVGFLEIGYQKELMYKHSYSYSAFGERDGN--GNTWLTAFVTKCFG	3198
Sbjct:		+ LT EI+S+A+G+L GYQ++L YKH +CSYS FGER G GNTWLTAFV K F	
	991	NETQQLTPEIKSKAIGYINTGYQRLNYKHVDGYSYTFGERYGRNQGNWLTAFVLKTF	1050
Query:	3199	QAQKFIIDPKNIQDAIKWMAGNQLPSGCVANVGNLLHTAMKGGVDEVSLETAATAALL	3378
Sbjct:		QA+ +IFID +I AL W++ Q +GC+ + G+LL+ A+KGV+DEV+L+AY+T ALL	
	1051	QARAVIFIDEAHITQALIWLSQRQKDNCGFRSSGSLINNAIKGGVEDEVTLTSAITIAL	1110

Fig. 2B

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

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Query: 3379 EMGKDVDDPMVSGQLRCLKNSATST-----TNLYTQALLAYIFSLAGEMDIRNILLKQ 3537
      E+ V P+V L CL+ SA T +++YT+ALLAY F+LAG D R +LK
Sbjct: 1111 EILLTVTHPVVRNALFCLE-SAWKTAQEGDHGSHVYTKALLAYAFALAGNQDKRKEVLKS 1169

Query: 3538 LDOQAIISGESIYWSQKPTPSNASPWSEPA--VDVELTAYALLAQLT-KPSLTQKEIA 3708
      L+++A+ S++W + P + + EP A +VE+T+Y LLA LT +P+ T +++
Sbjct: 1170 LNEEAVKDNSVHWERPQKPKAPVGHFYEPQAPSAEEMTSYVLLAYLTAQPAPTSEDLT 1229

Query: 3709 KATSIWAWLAKQHNAYGGFSSQTDTVVALQALAKY-ATTAYMPSEEEINLVVKSTENFQRT 3885
      AT+IV W+ KQ NA GGFSSQ TVVAL AL+KY A T + + ++S+ F
Sbjct: 1230 SATNIVKWIITKQNAQGGFSSQTHTVVVALHALSKYGAATFRTGKAAQVTIQSSGTFSSK 1289

Query: 3886 FNIQSVNRLVFQODTLNVPNGMYTLEASGQGCYVYQTVLRYNILPPTNMKTFSLSVEIGK 4065
      F + + NRL+ QQ +LP +PG Y+++ +G+GCVY+QT L+YNILP F+L V+
Sbjct: 1290 FQVDNNRLLLQQVSLPELPGEYSMKVTGEGCVYLQTSKYNILLPEKEEFFFALGVQTL 1349

Query: 4066 ARCEQPTSPRSLTLTIHTSYVGSRSSNNMAIVEVKMLSGFSMEGTNQLLQQPLVKKVE 4245
      C++P + S +++ SY GSR+SNMAIV+VKM+SGF P++ T ++L + V + E
Sbjct: 1350 QTCDEPKAHTSFQISLSVSYTGSRSASNMAIVDKMVS GFIPKPTVKMLERSNHVSRTE 1409

Query: 4246 FGHTDLNIYLDLIKNTQTYTFTISQSVLVTNLKPATIKVVDYVYLPGSFKLSQY 4407
      ++ + IYLD++ T + FT+ Q V V +LKPA +KVVDY F +++Y
Sbjct: 1410 VSSNHVLIYLDKVSNTLSLFTTVLQDVPVRDLKPAIVKVDYVYETDEFAIAEY 1463

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FIG. 2C

BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH OVOS_CHICK OVOSTATIN PRECURSOR SEQ ID NO: 41

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 29)
 Subject: >sp|P20740|OVOS_CHICK OVOSTATIN PRECURSOR (OVOMACROGLOBULIN) >pir||A20872 ovostatin precursor - chicken
 >emb|CAA55384.1|(X78801) ovomacroglobulin, ovostatin [Gallus gallus] (SEQ ID NO: 41)
 length = 1473

Score = 1300 (462.7 bits), Expect = 6.1e-135, Sum P(2) = 6.1e-135
 Identities = 297/849 (34%), Positives = 457/849 (53%), Frame = +3

Query: 96 VYKFPVSPTRKMAQLLLGLMLALSPAIAEEL-PNYLVTLERLNFPSVQKVCIDLSPGYS 272
 + F ++ KMW + +L +L L A +E P Y++ +PA L S +VCL
 Sbjct: 9 ILSFFCLTVRKMWLKFILAILLHAAAGKEPEQYVLMVAVLQSDSPSQVCLQFFNLNQ 68

Query: 273 DVKFTVTLETDKTKQLLEYSGLKKRHLHCISFLVPPPPAGGTEEVATIRVSGVGNNISFE 452
 + V LE + E + L C++F++PP + +A I + G +
 Sbjct: 69 TISVRVLEYDTINTTIFEKNITTSNGLQCLNFMIPPVT--SVSLAFISFTAKGTTFDLK 126

Query: 453 EKKKVLIIQRQNGTFFVQTDKPLYTPGQQVYFRIVTMDSNFVNDKYSVMVELQDPNSNRI 632
 E++ V+I + FVQTDKP+Y PGQ V FR+V +D NF PV + Y ++ +QDP +NRI
 Sbjct: 127 ERRSVMIWMMESFVQTDKPIYKPGQSVFRVVALDFNFKPVQEMYPLIAVQDPQNNRI 186

Query: 633 AQWLEVVPEQGIVDLSFQLAPEAMLGTYTVAAE--G-KTGFSTFVEEYVLPKFKVEVVE 803
 QW V E IV + F L E +LG Y + V + G +T +F VEEYVLPK F V
 Sbjct: 187 FQWQNVTSINIVQIEFPFLTEEPILGNKYIIVTKKSGERTSHSFLVEEYVLPKFDVTVTA 246

Query: 804 PKELSTVQESFLVKICCRYTYGKPMLGAVQSVSCQKANTYVYREVEREQLPDKCRNLSGQ 983
 P L+ + VKIC YTYG+P+ G VQ+SVC+ ++Y R + C++ +
 Sbjct: 247 PGSLTVMDSSELTVKICAVTYTGQPVVEGKVLQSVCRDFDSYG-----RCKKSPVCQSFTKD 301

Query: 984 TDKTGCFSAPVDMATFDLIGYAVSHQINIVATVVEEGTGVEANATQNIYISPMGSMTFE 1163
 D GC S + F+L Y +++ A V E+ ATQ+I I+ M S+ FE
 Sbjct: 302 LDTDGCLSHILSSKVFELNRIGYKRNLDVKAIVTEKEQVCNLTATQSIISITQVMSSLQFE 361

Query: 1164 DTSNFYHPNFPFSGKIRVRGHDDSLKHLVFLVIYGTNGTFNQTLVTDNNGLAPFTLET 1343
 + + Y P+ G+I++ D+S + N ++ L + N T N T TD NG+APF++T
 Sbjct: 362 NVDHHRRGIPYFGQIKLVKDNKSPISNKVIQLFVNKN--THNFT--TDINGIAPFSIDT 418

Fig 3A

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
OVOS_CHICK_OVOSTATIN_PRECURSOR_SEQ ID NO: 41**

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Query: 1344 SGWNGTDVSLGKQFQMEDLVYNPEQVPRVYQNAYLHLRPFYSTTRSFGLGIHRLNGPLKCG 1523
      S ++SL+ ++ D ++ + Y +A L ++ YS T SF+ I L + CG
Sbjct: 419 SKIFDPELSLKALYKTSQCHSEGWIEPSYDASLSVQRLYSWTSSFVRIEPLWKDMSCG 478

Query: 1524 QPQEVLDVYIDPADASPDQEIISFSYLLIGKGLVMEQKHLNKKKGLKASFSLSLTFT 1703
      Q + + V Y ++ ++F Y + KG +V+ G+ +N + +F + L
Sbjct: 479 QKRMITVYYILNTEGYEHINIVNFYVGMAGKIVLTGEIKVNIQADQ-NGTFMIFLVVN 537

Query: 1704 SRLAPDPSLVIYAIFPPSGGVVADKIQFSVEMCFDQNVSLGSPSQQLPGAELVQLQAAP 1883
      ++AP L++Y + P+ +VAD ++FS+E CF N+V L FS Q L + V L ++AA
Sbjct: 538 EKMAPALRLVYMLHPAKELVADSVRFSEIKCFKKNVQLQFSEKQMLTTSNVSLVIEAAA 597

Query: 1884 GSLCALRAVDENVLLLRPDRELNSRVSVMFPFHYQVQVAEYDQCVPVSGPWDFPQPL 2063
      S CA+RAVD+S+LLL+ + ELS ++Y + P Q ++ + D PQ
Sbjct: 598 NSFCRAVRAVDKSMILLKSETELSAETIYNLHPI----QDLQYIFNGLNLE---DDPQ-- 648

Query: 2064 IDPMPQGHSS-QRSIIWRPFSFSE-GTDLFSFTRDVGLKILSNAKIKKPVDCSH---RSPE 2228
      DP + + +RP S G D++ F RD+G+K +N+KI+P C+ R P
Sbjct: 649 -DPCVSSDDIFHKGLYRPLTSGLGPDVYQFLRDMGMKFFFTNSKIRQPTVCTRETVRPPS 707

Query: 2229 YSTAMG--AGGHPH-----AFESSTPLHQAEVSQVRQYFPETWLDLFPIGNSGKEAVH 2387
      Y G A H + A E H E +R++FPETW+WD+ I ++GK +V
Sbjct: 708 YFLNAGFTASTHVVKLSAEVAREERGRHILET--IREFFPETWIDWIIILINSTGKASVS 765

Query: 2388 VTVPDAITEWKAMSFCTSQSRGFGLSPTVGLTAPKPPFFVDLTLPYSVVRGESFRLTATIF 2567
      T+PD ITEWKA +FC + GFG+S LTAP+PFFVDLTLPYS++ GE F + A +F
Sbjct: 766 YTIPDTITEWKASAFCEELAGFGMSVPAITLTAQPFFVDLTLPYSIIHGDFLVRANVF 825

Query: 2568 NYLKDCIRV 2594
      NYL CI++
Sbjct: 826 NYLNHCIKI 834

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Fig 3B

BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 29)
 Subject: sp|R11334|R11334 Recombinant human alpha-2 macroglobulin. SEQ ID NO: 24
 Length = 1474

Score = 1289 (458.8 bits), Expect = 5.6e-134, Sum P(2) = 5.6e-134
 Identities = 300/834 (35%), Positives = 448/834 (53%), Frame = +3

Query: 141 LLLGMLALSPAIAEELPNVLVTLPARLNFPSVQKVCVLDLSPGYSDVKFIVTLETKDKTQK 320
 LLL +L + A P Y+V +P+ L+ +K C+ LS V + +LE+ +
 Sb|ct: 13 LLLLVLVPTDASVSGKPQYMLVPSLLHTTEKGCVLLSYLNETVTVSASLESVRGNRS 72
 Query: 321 LLEYSGLKKRHLHCISFLVPPAGGTEEVATIRVSGVGNNISFEKKKVLIRQNGTFFV 500
 L + LHC++F VP + EEV + V G F+++ V+++ + + FV
 Sb|ct: 73 LFTDLEAENDVLHCVAFAVPK--SSNEEVMTLVQVKGTQEFKKRTTVMVKNEDSLVFV 131
 Query: 501 QTDKPLYTPGQQVYFRIVTMDNSFVPVNDKYSVMVELQDPNSNRIAQWLEVVPEQGIVDLS 680
 QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIAQW E G+ S
 Sb|ct: 132 QTDKSTYKPGQTVKFRVWMDNFHPLNELIPLVIYIQDPKGNRIQWQSFQLEGGKQFS 191
 Query: 681 FQLAPEAMLGTYTVAVAE---GKTFTGSVEEVVLPKFVVEVPKELSTVQESFLVKIC 851
 F L+ E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ +E V +C
 Sb|ct: 192 FPLSSEPFQGSYKVVVQKKSGGTEHPFTVEEFVLPKFVQVTVVPKIITILEEMNVSV 251
 Query: 852 CRYTYGKPMGLGAVQSVQCQKANTYVYREVEREQLPDKCRNLSGQTDKTCGFSAPVDMATF 1031
 YTYGKP+ G V VS+C+K + + E C SQG + GCF V F
 Sb|ct: 252 GLTYGKPVPGHVTVVICRYSDA--SDCHGEDSQAFCEKFSGQLNSHGCFYQQVKTQVF 309
 Query: 1032 DLIGAYSHQINIVATVVEEGTGVAEANATQNIYISPMGSMTFEDTSNFYHNPFFSGKI 1211
 L Y +++ A + EGT VE Q+ I+ + ++F + + PF G++
 Sb|ct: 310 QLKREYEMKLHTEAQIQEEGTVVVELTGRQSSSEITRTITKLSFVKVDSHFRQGIPIFFGQV 369
 Query: 1212 RVRGHDDSFLLKNHLVFLVIYGTNGTFNFQTLVTDNNGLAPFTLETSGWNGTDVSLGKFQM 1391
 R+ + N ++F I G + TD +GL F++ T+ GT +++ ++
 Sb|ct: 370 RLVDGKGVPIPNKVIF--IRGNEANYISNATTDHGLVQFSINTNMGTSLTVRVNYKD 427
 Query: 1392 EDLVNDEQVPYRYQNAYLHLRPFYSTTRSFGLGHRINGPLKCGQPQEVLDYIDPADA 1571
 Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++
 Sb|ct: 428 RSPCYQVQWVSEEHAAHTAYLVFSPSKSFVHLEPMSHELPCGHTQTVQAHYILNGGTL 487

Fig. 4A

BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24

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Query: 1572 SPDQEIISFSYLLIGKSLVMEGQKHLNKKKGLKASFSLSLTFTSRLAPDPPLVVIYAIFFP 1751
      +++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P
Sbjct: 488 LGLKKLSFYLLIMAKGGIVRTGTHGLLVKQEDMKGHFSISIPVKSADIAPVARILLIYAVLP 547

Query: 1752 SGGVADKIQFSVEMCFDQVSLGFSFSPSQQLPGAELVQLQAAPGSLCALRAVDSEVLIL 1931
      +G V+ D ++ VE C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENCLENKVDLSFSPSQSLPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1932 RPDRELSNRSVYGMFFFWYGHYPYQVAEYDQCPVSGPWDFPQPLIDPMPQGHSSQRSIIW 2111
      +PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KPAELSSASSVYNLLP-----EKDLTGFPGLN-DQDDEDCINRHNVIYINGITY 655

Query: 2112 RP-SFSEGTDLFSFFRDVGLKILSNAKIKKPVDCSH-----RSPE-----YSTAMGAG 2252
      P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSSSTNEKDMYSFLEDMLGKAFNTSKIRKPKMCPQLQYEMHGPEGLRVGFYESDV-MG 714

Query: 2253 GGHPEAFESSTPLHQAEDSQVRQYFPETWLDLFPIGNSGKEAVHVTVPDAITEWKAMSF 2432
      GH P H VR+YF ETW+WDL + ++G V VTVPD ITEWKA +F
Sbjct: 715 RGHARLVHVEEP-HT---ETVRKYFAETWIWDLVVVNSAGVAEVGVTVPTITENKAGAF 770

Query: 2433 CTSQSRGFGGLSPTVGLTAFKPFVVDLTLPYSVVRGESFRLTATIFNYLKD CIRV 2594
      C S+ G G+S T L AF+PFFV+LT+PYSV+RGE+F L AT+ NYL CIRV
Sbjct: 771 CLSEDAGLGISSTASLRAFQPFVVELTMPYSVIRGEAFTLKATVLNLYLPKCIRV 824

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Fig. 4B